IN THE CLAIMS:

Applicants, pursuant 37 C.F.R. § 1.121, submit the following amendments to the claims:

1. (Currently amended) A method for diagnosis or prognosis of esophageal cancer or Barrett's esophagous, Barrett's intestinal tissue, esophageal adenocarcinoma, esophageal dysplasia, esophageal metaplasia, and combinations thereof, ~~esophageal cancer-related conditions,~~ comprising:

(a) obtaining a esophageal tissue sample comprising genomic DNA;

(b) performing a methylation assay of the tissue sample, wherein the methylation assay determines the methylation state of at least one genomic CpG sequence, wherein the at least one genomic CpG sequence is located within the *MYOD1* gene CpG island sequence having both a frequency of CpG dinucleotides corresponding to an Observed/Expected Ratio >0.6, and a GC Content >0.5 that extends from nucleotide position 9,843 to 10,043 of SEQ ID NO:66; and

(c) determining, based at least in part upon the detection of hypermethylation ~~state~~ of the at least one genomic CpG sequence, a diagnosis or prognosis of esophageal cancer or Barrett's esophagous, Barrett's intestinal tissue, esophageal adenocarcinoma, esophageal dysplasia, esophageal metaplasia, ~~pre-cancerous conditions in normal esophageal squamous mucosa~~, and combinations thereof.

2. (Cancelled).

3. (Currently amended) The method of claim 1, wherein the *MYOD1* gene sequences are those delimited ~~defined~~ by the specific oligonucleotide primers ~~and probes~~ corresponding to SEQ ID NOS:7 and 8 ~~SEQ ID NOS:7-9~~, as listed in TABLE II, or portions thereof.

4. (Cancelled).

5. (Cancelled).

6. (Currently amended) The method of claim 1, comprising determining the methylation state of a plurality of genomic CpG sequence located within the MYOD1 gene CpG island sequence.

7. (Cancelled).

8. (Cuurently amended) The method of claim 6, wherein at least one of the CpG dinucleotide sequences is within a region delimited ~~defined~~ by the specific oligonucleotide primers and probes corresponding to SEQ ID NOS:7-9, as listed in TABLE II.

9. (Cancelled).

10. (Cancelled).

11. (Previously presented) The method of claim 1, wherein the condition is selected from the group consisting of esophageal adenocarcinoma, esophageal dysplasia, esophageal metaplasia, Barrett's intestinal tissue, and combinations thereof.

12. (Original) The method of claim 11, wherein the cancer is esophageal adenocarcinoma, and wherein making a diagnostic or prognostic prediction of the cancer, based upon the methylation state of the genomic CpG sequences provides for classification of the adenocarcinoma by grade or stage.

13. (Previously presented) The method of claim 6, wherein the cancer or cancer-related condition is selected from the group consisting of esophageal adenocarcinoma, esophageal dysplasia, esophageal metaplasia, Barrett's intestinal tissue, and combinations thereof.

14. (Original) The method of claim 13, wherein the cancer is esophageal adenocarcinoma, and wherein making a diagnostic or prognostic prediction of the cancer, based upon the methylation state of the genomic CpG sequences provides for classification of the adenocarcinoma by grade or stage.

15. (Original) The method of claim 1, wherein the methylation assay used to determine the methylation state of genomic CpG sequences is selected from the group consisting of MethylLight™, MS-SNuPE, MSP, COBRA, MCA, and DMH, and combinations thereof.

16. (Original) The method of claim 6, wherein the methylation assay used to determine the methylation state of genomic CpG sequences is selected from the group consisting of MethylLight™, MS-SNuPE, MSP, COBRA, MCA and DMH, and combinations thereof.

17. (Previously presented) The method of claim 1, wherein the methylation assay used to determine the methylation state of the at least one genomic CpG sequence is based, at least in part, on an array or microarray comprising CpG-containing sequences located within the *MYOD1* gene.

18. (Cancelled)

19. (Previously presented) The method of claim 17, wherein the *MYOD1* gene sequence is delimited ~~defined by, or correspond to~~ the specific oligonucleotide primers ~~and probes~~ corresponding to SEQ ID NOS:7 and 8 ~~SEQ ID NOS:7-9~~, as listed in TABLE II, or portions thereof.

20.-24. (Cancelled).